Root ubiquitinome under osmotic stress

Nathalie Berger, Vincent Demolombe, Sonia Hem, Valérie Rofidal, Laura Steinmann, Gabriel Krouk, Lionel Verdoucq, Véronique Santoni

Journées PROTÉOME VERT des 8 et 9 juin 2021
Visioconférence

Résumés / Abstracts

Programme

Mardi 8 juin

14h00 – 14h05 : Accueil
14h05 – 14h50 : **Sophie Colombié** (Biologie du Fruit et Pathologie, Bordeaux) : Estimer le turnover des protéines du fruit grâce à la transcriptomique et à la protéomique
14h50 – 15h10 : **Willy Bienvenut** (PAPPSO, Gif-sur-Yvette) : Sub-optimal ^{15}N metabolic labelling in plant to determine protein turnovers: A new look at the isotopic distribution
15h10 – 15h30 : **Emmanuelle Bancel** (GDEC, Clermont-Ferrand) : Proteomic and peptidomic tools combined with immuno–chemistry to analyze in vitro gastrointestinal digestibility of bread wheat

15h30 – 15h40 : Pause

15h40 – 16h00 : **Luciana de Oliveira** (PAPPSO, Gif-sur-Yvette) : SpecOMS, an open search approach challenging the identification of peptides showing sequence polymorphism
16h00 – 16h20 : **Maïté Leschevin** (BioEcoAgro, Amiens) : Mise en évidence d'une corrélation entre les caractères physiologiques, biochimiques de la réponse au stress salin chez Arabidopsis thaliana par une analyse protéomique quantitative par TMT
16h20 – 16h40 : **Gwendal Cueff et Loïc Rajjou** (IJPB, Versailles) : La germination : Un processus biologique pour améliorer les propriétés nutritionnelles et organolepiques des graines !?

Mercredi 9 juin

09h30 – 10h15 : **Steven Moussu** (Université de Lausanne) : Bases structurales et biochimiques de la reconnaissance des peptides de signalisation RALF par les protéines LRX de la paroi cellulaire, pour orchestrer le remodelage de la paroi cellulaire
10h15 – 10h35 : **Artur Pinski** (LRSV, Auzeville-Tolosan ; Université de Silésie, Katowice) : Comparison of mass spectrometry data and bioinformatics predictions to assess the bona fide localization of proteins in plant cell walls and at the plasma membrane surface
10h35 – 10h55 : **Hasan Kolkas** (LRSV, Auzeville-Tolosan) : A comparative proteomic study reveals specific features of Marchantia polymorpha cell wall proteome in terms of cell wall proteins diversity

10h55 – 11h05 : Pause

11h05 – 11h25 : **Véronique Santoni** (BPMP, Montpellier) : Root ubiquitinome under osmotic stress
11h25 – 11h45 : **Delphine Aimé et Karine Gallardo-Guerrero** (Agroécologie, Dijon) : Protéomique shotgun des graines de féverole : vers l'identification de protéines associées à la résistance aux bruches
11h45 – 12h05 : **Olivier Langella** (PAPPSO, Gif-sur-Yvette) : X!TandemPipeline, plus qu 'un pipeline

https://www6.inrae.fr/proteome-vert
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Root ubiquitinome under osmotic stress

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Osmotic stress is detrimental for the plant which survival relies heavily on proteomic plasticity. Protein ubiquitination is a central post-translational modification in osmotic mediated stress. Plants use the ubiquitin proteasome system to modulate protein contents required to respond to and tolerate adverse growth conditions and a role for ubiquitin to mediate endocytosis and trafficking of plant plasma membrane proteins has recently emerged. In this study, using the K-Ɛ-GG antibody enrichment method integrated with high-resolution mass spectrometry, a list of 786 ubiquitinated lysine (K-Ub) residues in 451 proteins of which 50 % were transmembrane proteins was compiled for Arabidopsis root membrane proteins, increasing the database of ubiquitinated substrates in plants. Ubiquitination particularly occurred within membrane proteins and the protein machinery involved in their internalization and sorting. Despite absence of identification of a strict ubiquitination motif, the presence of acidic residues close to K-Ub was evidenced. *In silico* interactomics analysis allowed to suggest two E2 ligases, UBC32 and UBC34 to target ubiquitination of membrane proteins. This study also showed a decrease of NRT2;1 with osmotic stress treatment, putatively mediated by its decreased ubiquitination, correlating with an increased NO_3^- influx. Then, this study revealed that a major plasma membrane aquaporin (PIP2;1) harbors two ubiquitination sites that may interfere with N-terminal acetylation and C-terminal phosphorylation, to putatively contribute to a decreased root hydraulic conductivity.